CLAIM AMENDMENTS

1-12. (canceled)

13. (currently amended): A method to design primers ~~to~~ wherein said primers target a first nucleotide sequence ~~that~~ which first nucleotide sequence results in at least one phenotypic characteristic, the method comprising the steps of:

providing a second nucleotide sequence that is known to result in the phenotypic characteristic;

comparing the second nucleotide sequence to nucleotide sequences cataloged in one or more databases that ~~correlate~~ annotate nucleotide sequences with phenotypic characteristics;

extracting any cataloged ~~gene~~ nucleotide sequences that contain a portion of the second nucleotide sequence and which ~~result in~~ are annotated with said phenotypic characteristic;

aligning the second nucleotide sequence to each extracted ~~gene~~ nucleotide sequence;

prioritizing the extracted ~~gene~~ nucleotide sequences based on identity match and percent similarity with sequences having the highest identity match and highest percent similarity being highest in priority to ensure alignment to the second nucleotide sequence; and

designing one or more primers based on matching portions of the ~~alleged~~ aligned prioritized sequences to target said first nucleotide sequence.

14. (currently amended): The method of claim 13, further comprising the step prior to the step of designing said primers of filtering the extracted nucleotide sequences to eliminate portions ~~common to unwanted genes~~ which are regions commonly found in encoding nucleotide sequences.

15. (canceled)

16. (currently amended): The method of claim 13, further comprising the step of cloning ~~genetic material~~ said first nucleotide sequence using the one or more designed primers.

17. (previously amended): The method of claim 13, wherein the one or more databases are selected from cataloged sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

18. (canceled)

19. (previously amended): The method of claim 13, wherein the one or more primers are nested.

20-22 (canceled)

23. (previously amended): The method of claim 13, wherein the step of prioritizing the extracted nucleotide sequences to ensure the alignment of the selected nucleotide sequences is accomplished by using a statistical analysis of the alignment.

24. (canceled)

25. (previously amended): The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

26. (previously amended): The method of claim 13, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing the nucleotide sequences.

27-33 (canceled)

34. (currently amended): A system for designing primers ~~to~~ which primers target a first nucleotide sequence ~~that~~ which first nucleotide sequence results in at least one phenotypic characteristic comprising:

one or more computers collectively having program means thereon for performing the method of claim 1; and

one or more databases containing the cataloged gene sequences; and

a communication link connecting the computer or computers to said one or more databases.

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35. (canceled)

36. (currently amended): The system of claim 34, wherein the program means filters the extracted nucleotide sequences to eliminate portions ~~common to unwanted genes~~ which are regions commonly found in encoding nucleotide sequences.

37. (canceled)

38. (previously amended): The system of claim 36, further comprising an apparatus that clones genetic material using one or more primers.

39. (previously amended): The system of claim 36, wherein the one or more databases are selected from cataloged gene sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

40. (previously amended): The system of claim 36, wherein the phenotypic characteristic is expression in insect mid-gut epithelium.

41. (previously amended): The system of claim 36, wherein the one or more primers are nested.

42-44 (canceled)

45. (previously amended): The system of claim 36, wherein the program means uses a statistical analysis of the alignment of the second nucleotide sequence to prioritize the extracted sequences.

46. (canceled)

47. (previously amended): The system of claim 36, wherein the selected gene sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

48. (previously amended): The system of claim 36, wherein the second nucleotide sequence is aligned to each extracted gene sequence by comparing nucleotide sequences.

49-59 (canceled)

60. (currently amended): A computer program embodied on a computer-readable medium for designing primers ~~to~~ wherein said primers target a first nucleotide sequence ~~that~~ which first nucleotide sequence results in at least one phenotypic characteristic, said computer program comprising:

means for providing a second nucleotide sequence that results in the phenotypic characteristic;

means for providing at least one database containing ~~cataloged~~ nucleotide sequences cataloged therein wherein said catalog ~~correlates sequence~~ annotates said sequences to resulting phenotypic characteristics;

means for extracting from said at least one database a plurality of cataloged nucleotide sequences containing a portion of the said second nucleotide sequence and which are annotated with said phenotypic characteristic;

means for aligning said second nucleotide sequence with said cataloged gene sequences;

means for prioritizing the extracted gene sequences based on identity match and percent similarity with sequences having the highest identity match and highest percent similarity being highest in priority to ensure alignment with the second nucleotide sequence; and

means for designing one or more primers based on matching portions of the aligned prioritized sequences to target said first nucleotide sequence.

61. (currently amended): The computer program of claim 60, further comprising a code segment for filtering the extracted nucleotide sequences to eliminate portions which are regions commonly found in encoding nucleotide sequences.

62-63 (canceled)

64. (previously amended): The computer program of claim 60, wherein the one or more databases are selected from cataloged gene sequences for humans, rats, mice, zebra fish, frogs, Drosophila, nematode, C. elegans, mosquito and bacteria.

65. (previously amended): The computer program of claim 60, wherein the phenotypic characteristic is expression in insect mid-gut epithelium.

66. (previously amended): The computer program of claim 60, wherein the one or more primers are nested.

67-69 (canceled)

70. (previously amended): The computer program of claim 60, wherein the code segment for prioritizing the extracted nucleotide sequences based on alignment with the second nucleotide sequence is accomplished by using a statistical analysis of the alignment.

71. (canceled)

72. (previously amended): The computer program of claim 60, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced amino acid sequences.

73. (previously amended): The computer program of claim 60, wherein the second nucleotide sequence is aligned to each extracted nucleotide sequence by comparing deduced nucleic acid sequences.

74-80 (canceled)

81. (currently amended): An article of manufacture comprising a computer medium having the computer readable program code ~~means~~ of claim 60 embodied therein.

82. (previously amended): The article of manufacture of claim 81, wherein said medium is:

a server, a hard drive, a CD-ROM or a diskette.